AMENDMENTS TO THE CLAIMS

The listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

Claims 1-15 are canceled.

16. (Currently amended) A method for identifying polymorphic markers in a population, comprising the steps of:

~~characterizing~~ selecting a first and second individual ~~sample that includes~~ from a plurality of individuals ~~from~~ of the population;

providing a ~~representative~~reference genomic DNA microarray;

~~selecting an individual from the first sample~~;

hybridizing genomic DNA of each of the first and second individuals to the ~~selected individual with the representative~~ reference microarray;

determining segments of hybridization between the genomic DNA of each of the first and second individuals ~~selected individual~~ and the ~~representative~~ reference microarray;

calculating a hybridization intensity ratio for each hybridized and non-hybridized segment;

converting each intensity ratio into a ~~numerical element~~ binary digit consisting of a 0 or 1 bit such that each segment of the reference microarray is represented by a 0 or 1 bit;

compiling data consisting of the numerical elements to produce a bit string for each individual, each bit string having the same total number of bits and each bit having a unique position common to both strings; and

analyzing the data to identify patterns of hybridization present in the population, wherein the relatedness of the bit strings is determined by comparing the value of each bit within the bit string of the first individual to the value of each bit within the bit string of the second individual.

17. (Currently amended) The method of claim 16, wherein the ~~representative~~ reference microarray is fabricated from genomic DNA from an individual in the population.

18. (Currently amended) The method of claim 16, wherein the step of selecting [[an]] a first individual from the first sample involves selecting an individual that shares the most characteristics among other individuals of the same population.

19. (Currently amended) The method of claim 16, further comprising the step of hybridizing genomic DNA from each of the individuals in the first sample to the representative population to the reference microarray to determine genetic relatedness of the all of the individuals from the population first sample.

20. Canceled.

21. (Currently amended) The method of claim 20 16, wherein at least one of the first and second samples individuals is characterized by genotype, and at least one of the individuals selected from the first and second samples is selected based upon the genotypic characterization.

22. (Currently amended) The method of claim 20 16, wherein at least one of the first and second samples individuals is characterized by phenotype, and at least one of the individuals selected from the first and second samples is selected based upon the phenotypic characterization.

23. (Original) The method of claim 18, further comprising the step of labeling the genomic DNA of each selected individual with a fluorescent dye.

24. (Original) The method of claim 23, wherein the genomic DNA of each selected individual is labeled with a different fluorescent dye.

25. (Original) The method of claim 23, wherein the step of determining each segment's hybridization intensity includes determining the fluorescent intensities of the hybridized segments.

Claims 26 to 28 are canceled.

29.   (Currently amended) The method of claim 28, further including the step of collecting the bit string for each individual ~~in the sample~~ into a composite file.

30.   (Original) The method of claim 29, wherein the step of analyzing further includes normalizing the data through mean and median centering of each of the hybridization intensity ratios.

31.   (Original) The method of claim 29, further including the step of preparing a graphical representation for each bit string.

32.   (Original) The method of claim 16, wherein the population is a bacterial population.

33.   (Original) The method of claim 32, wherein the bacterial population is selected from the group consisting of *Listeria monocytogenes, Escherichia coli, Lactobacillus casei, Lactobacillus lactus, Salmonella typhimurium, Salmonella entereditis*, and *Salmonella typhi*.

34. (Withdrawn) A method for identifying polymorphic markers in a bacterial population comprising a plurality of individuals, involving the steps of:

    providing a plurality of bit strings, each string representing an individual within the population and having the same number and position of bits, each bit having a value of 0 or 1;

    generating a graphical representation of the relatedness of the bit strings, the graphical representation including selectable elements;

    selecting a first selectable element;

    selecting a second selectable element; and

    identifying bits that are present in each bit string representing the first selectable element and absent in each bit string representing the second selectable element, or bits that are absent in each bit string representing the first selectable element and present in each bit string representing the second selectable element.

35. (Withdrawn) The method of claim 34, wherein the relatedness of the bit strings is determined by the commonality of bit values at corresponding positions in the bit strings.

36. (Withdrawn) The method of claim 34, wherein the graphical representation is a dendrogram and the selectable elements are leaves and nodes, each leaf representing a single bit string, and each node representing two or more bit strings.